Figure 1

IDENTIFIED LAB mRNA SEQUENCES

BOLD

CGGGAGCTTG**AAGGA**CACAAGAATGGGAGGAAAGGCGGACTCTCAGGAAC (Ribosome Binding Site)
TTCATTCTTCACGTGGTTT**ATG**GTGATTGCATTGCTGGGCGTCTGGACAT (Start Codon)
CTGTAGCTGTCGTTTGGTTTGATCTTGTTGACTATGAGGAAGTTCTAGGA
AAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGTGGATGA
TGCCAAAGTTTTATTAGGACTTAAAGAGAGATCTACTTCAGAGCCAGCAG
TCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCCGAGGAGCAGGTTCCT
GTGGAGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCA
GTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACT
TGCAACAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGATGAG
TTTCTTATGGCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCTGA
AGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGACAGTTT
CACAAGACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAAT
CCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATAC
AGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTC
TAGAAAATGAAGGGATAGAAATCACAGAAGTAACTGCTCCCCCTGAGGAT
AATCCTGTAGAAGATTCACAGGTAATTGTAGAAGAAGTAAGCATTTTTCC
TGTGGAAGAACAGCAGGAAGTACCACCAGATACT**TAA**AGCTTCAAAAAGA (Stop Codon)
CTGCCCCTACCACCACAGGAGGACCAGCCTAACCATACGCTCCAAAAGAT
GGCTGTGATAGATCTTGTGAAGCAATTACTGAGCAGATCAAGATCTTTGG
GAAGGAACACTAAAGATGTTTTGAATGAATTATAGTCCACTGGCATTTTA
GTGTATTTTTTTTTCTTTTTAGAAACACACATTTCTAAAAATGTCATGTT
ACATTCCTGCATGTCCCTTTTGATAGCATTAGTGGATCCATTGGATTTCT
TTTTTCTTTTTGTGAGACAGCTTTTAGTCTTACCTGA**ATTTA**TGTGTGTT (Instability Sequence)
TTTCCGACAGTGGTTAATAATTATATTGGTGATGTAGCAGCAATTGTGTT
GGCAGGGTTTTCATATATTATTAGTAATTAACACTAACTGTTGGACTGAC
TTGTGTACACTGTGTTAAACATG**ATTTA**AAAGCTATTAAGAGTACTTTGT (Instability Sequence)
GTTAGCACTCTTAAAAACGCTAACAGAGATCATCATTAGCTGTGAAGATT
TGAGTTGTATATACCTGCACTGATATTCTTATCAAAAATTTCTACATTAG
CTTTAAGTGTTCAGATTAACACTTTTGAAACCTTTGTAGCTTTTAGCTGA
TTAATTAGAAAAATTAATATTTCAGTGAAAGTTTTAAATTATC**ATTTA**TT (Instability Sequence)
TATTTTTTTAAATGAGAGGGGAAAGCTGAAATTCCTTGTTAAGACACAAG
GAAAAGAATGGCCCTACTATTATCATGCAAAAATGCTTTGTTGGCACCT
CAGATTAATCATATAATAGCTATAGTCTCTTCAGCATTTGTTTAAATTTT
AGAAACCTGTATAAATTACTGGTGCATAACTTAAAGATTATTCTGCCTT
TGGCTAATTGAGTAATTCCCCTCCAGCACTAGAGACCGCTCAGTGCTCTT
ACTAGATGAACTCAGTAACGCCTTGAGCTGGGTTGATTGAGGATGTGTGA
AAAAGCTCACAGAGCCCGATGCCTGCTGCTATTTCACGGCAATGAGCCTT
TTTCTTTCTACACTGAAGATTTTCTTCTT**ATTTA**ATGTGGTTATTTTGG (Instability Sequence)
GCTCAGAAATAATTGCTCTGTTGAAAATAATCCTTTGTCAGAAAAGAAGG
TAGCTACCACATCATTTTGAAAGGACCATGAGCAACTATAAGCAAAGCCA
TAAGAAGTGGTTTGATCGATATATTAGGGGTAGCTCTTGATTTTGTTAAC
ATTAAGATAAGGTGACTTTTTCCCCCTGCTTTTAGG**ATTAAAA**TCAAAGA (Sub-optimal Poly-
TACTTCTATATTTTTATCACTATAGATCATAGTTATTATACAATGTAGTG   adenylation Site)
AGTCCTGCATGGGTACTCGATGTGTAATGAAACCTGAAATAATAATAAGA
TAATAAGAAAAGCAATAATTTTCTAAAGCTGTGCTGTCGGTGATACAGAG
ATGATACTCAAATTAT**AATAAA**CTCTTCATTTTGTGAATTATAGAAGCT (Optimal Polyadeny-
ACTTTTTATAAAGCCATATTTTTTTAGGGAAACTAAGGAGTGACATAGAA   lation Site)
CTGATGAATGAGTAAAAGTAAGTTTTGCTGGATTTTTGTAGAACTCTGGA
CGTTGAGGATTCATTATGCTGTGGTTAACTTTAAATATTTTT

Figure 2

COMPUTER PREDICTED DOMAINS
IN LABYRINTHIN

MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLK

ERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAE

HVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHV

EETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDvtyqvyeeqavY
                                        <--MAD I-->

EPLENEGIEITEVTAPPEDNPVEDSQviveevsifpvEEQQEVPPDT
                      <--MAD II->

Predicted Ca⁺⁺ Binding Region

                              VLGKLGIYDADGDGDFDVDDAKVLLGLK

Parvalbumin   vkkafaildqdksgfieedelklflqnf
Calmodulin   fkeafslfdkdgdgtittkelgtvmrsl
Troponin-C   ladcfrufdknadgfidieelgeilrat

Ca⁺⁺ Binding Residues   * * *   * *
Required residue   +
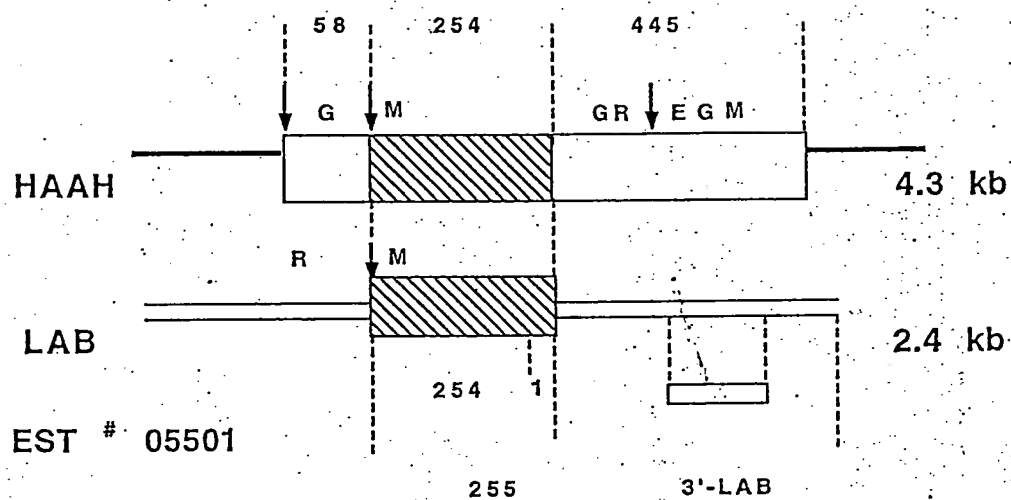
SYMBOL KEY

BOLD = Eukaryotic Leader Sequence

_____ = Myristylation site
^

lower case = Membrane Anchoring Domian (MAD)
<-------->

= Start Colon
R = Ribosome Binding Site
E = Enzymatic Site
G = Glycosylation Site
M = Membrane Anchoring Domain
3'-LAB = Contains poly A signal (x2); instabilty sequence (x4)